Deep marine subsurface archaeal communities of the Peru Trench: Sulfate-reducers, Methanogens, and Unknowns

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Community composition of methanogens and sulfate-reducers was studied in cold, organic-rich sediments of the Peru Trench, collected by the Ocean Drilling Program in 2002 (Leg 201, site 1230). We used PCR assays targeting functional genes of methanogens (mcrA) and sulfate reducers (dsrAB) throughout the sediment column. Methanogen-specific DNA was successfully amplified from a sample at 44.3 mbsf that coincided with a local acetate peak. Sequences fell into a novel cluster, with members of the obligately acetoclastic *Methanosaeta* group as closest cultured relatives. Sequences of sulfate-reducing prokaryotes were obtained from surface sediments and shared highest similarity with cultured members of the archaeal order *Archaeoglobales*.

We searched for unequivocal evidence of metabolically active Archaea by cloning reverse-transcribed 16S rRNA sequences that had been amplified with general archaeal 16S primers, and 16S primers specific to suspected anaerobic methanotrophs (ANME-2). Preliminary BLAST searches of general archaeal sequences from various depths (0-124 mbsf) revealed active populations of Deep-Sea Archaeal Group (DSAG) and Marine Benthic Group-D (MBG-D). None of the detected archaeal groups had closely related cultured representatives. Suspected anaerobic methanotrophic sequences were amplified successfully from several cores in the methane-sulfate transition zone of Site 1230.

The dominance of uncultured archaeal lineages (DSAG, MBG-D) in the Site 1230 clone libraries contrasts with relative scarcity of recognizable methanogens and sulfate-reducers. These uncultured archaeal subsurface lineages do not share the classical key genes of methanogenic and sulfate-reducing pathways (mcrA and dsrAB), and represent novel deep subsurface organisms with unknown physiology. Our results substantiate the existence of a systematically distinct archaeal community in the deep marine subsurface.